

SEQUENCE LISTING

<110>		M, LONNIE SHENGDE								
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		ccttgccgaa								
		ctgaagaagc								
		ttcagggcgg								0
gcctto	gcgct	gccataatga	agcagcctc	c gg	gtgttttgg	caga	itttaag	cgctgcctga	a 36	50
ttttcg	gtgat	cctctagagt	ctatgaaat	g ga	agattcatt	tatg	jectete	tcttattcg	g 42	20
ataaco	catcc	agtcatccgc	aagcttggc	C					45	0
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<220>

<223> Description of Artificial Sequence: Synthetic expression vector

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<212> DNA
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<400> 4
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<213> Artificial Sequence

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<222> (7061)..(8251)
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gcatggacat cccagacatt gggattgaac ctgtttggtg tcatgctttt gattacgact
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                                                                      240
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                                                                      480
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                                                                      540
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	agc ctt gcc Ser Leu Ala 35		_			1586
	tcc gtt agc Ser Val Ser 50					1634
	gcc ggc aac Ala Gly Asn 65					1682
	ttc tac aca Phe Tyr Thr					1730
	agc att gtt Ser Ile Val		Met Gly			1778
	cag gac ccg Gln Asp Pro 115	Ala Gly Asn				1826
	gca atc gcc Ala Ile Ala 130					1874
	gca gaa aac Ala Glu Asn 145		Glu Ala	_	-	1922

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				_			_			_		acc Thr 185					2018	
7												gac Asp				_	2066	
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										_		acg Thr	_				2162	
												gcc Ala	_	_			2210	
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2	Asp 270	Gly	Asn	Gly	Gly	Val 275	Asn	Gln	Thr	Asp	Thr 280	gac Asp	Ala	Trp	Val	Thr 285	2306	
F	?he	Met	Arg	Asp	Asn 290	Asn	Ile	Ser	Asn	Ala 295	Asn	tgg Trp	Ala	Leu	Asn 300	Asp	2354	
I	'nуs	Ser	Glu	Gly 305	Ala	Ser	Thr	Tyr	Tyr 310	Pro	Asp	tct Ser	Lys	Asn 315	Leu	Thr	2402	
G	31u	Ser	Gly 320	Lys	Ile	Val	Lys	Ser 325	Ile	Ile	Gln	agc Ser	Trp 330	Pro	Tyr	Lys	2450	
A	Ala	Gly 335	Ser	Ala	Ala	Ser	Thr 340	Thr	Thr	Asp	Gln	tca Ser 345	Thr	Asp	Thr	Thr	2498	
M 3	Met 850	Ala	Pro	Pro	Leu	Thr 355	Asn	Arg	Pro	Gln	Pro 360	aca Thr	His	Arg	Gln	Thr 365	2546	
				Cys								tgg Trp					2594	

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tgg gcg ggc cgg cag cga ctc ata acg a Trp Ala Gly Arg Gln Arg Leu Ile Thr L 385 390	
aca aag gga acc tgt ata ccg caa act g Thr Lys Gly Thr Cys Ile Pro Gln Thr G 400 405	
gca gcg att cct cct ggg cac agg ttg g Ala Ala Ile Pro Pro Gly His Arg Leu V 415 420	
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tacceaactt aategecttg cagcacatec coctttegec agetggegta atagegaaga 4415 ggecegeace gategeett cecaacagtt gegeageetg aatggegaat ggegeetgat 4475 geggtatttt ctecttaege atetgtgegg tattteacac egeataggeg egeetatggt 4535 geacteteag tacaatetge tetgatgeeg catagttaag ceageeega caceegeeaa 4595 caceegetga egegeetga egggettgte tgeteeegge ateegettac agacaagetg 4655 tgaeegtete egggagetge atgtgteaga ggtttteace gteateaceg aaacgegega 4715 gaegaaaggg cetegtgata egectattt tataggttaa tgteatgata ataatggttt 4775 cttagaegte aggtggeact ttteggggaa atgtggegg aaccectatt tgtttattt 4835 tetaaataca tetaaatatg tateegetea tgagacaata accetgataa atgetteaat 4895 aatattgaaa aaggaagagt atg agt att caa cat tte egt gte gee ett att Met Ser Ile Gln His Phe Arg Val Ala Leu Ile 430 aatattgaaa aaggaagagt atg agt ett eet gtt ttt get cac eea gaa acg 4996 Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr 440 ats 445 ctg gtg aaa gta aaa gat get gaa gat cag ttg ggt gea ega gtg ggt 5044 Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly 485 tee daa etc gaa etg gat ete aac age ggt aag atc ett gag agt ttt ege 7992 Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg 485 cee gaa gaa egt ttt cea atg atg age act tt aaa gt etg ege 619 Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Glu Gln Leu Cys 500 gge geg gta tta tee egt att gae gee ggg caa gag caa ete ggt ege 619 Ala Val Val Eys Asp Ala Gly Gln Glu Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Gly Arg 505 ege gas at tta tee egt att gae gee ggg caa gag caa ete ggt ege 619 Ala Val Val Val Sap Ala Gly Gln Glu Glu Gln Leu Gly Arg 505 ege geg gta tta tee egt att gae gee ggg caa gag caa ete ggt ege 619 Ala Val Val Val Sap Ala Gly Gln Glu Glu Gln Leu Gly Arg 505 ege ata cac tat tet cag aat gae ttg ggt gag tae tea ca ca gte aca 621 Ala File His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr 520 gga aaa cat ett acg gat gge atg aca gat acg at ta teg egt ggt 610 Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala	מתחתחתחתו	nn nnnnnnnnn	nnnnnnnnn	nnnnnnnn	nnnnnngatc ctctagagt	c 4295
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Met Ser Ile Gln His Phe Arg Val Ala Leu Ile 430 CCC ttt ttt gcg gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg 4996 Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr 440 Ctg gtg aaa gta aaa gat gct Ala Glu Asp Gln Leu Gly Ala Arg Val Gly 455 Ctg gtg aaa ctg gat ctc aac agc ggt aag at ctt ggt gcd Glu Arg Val Gly 455 Ctg gaa gaa ctg gat ctc aac agc ggt aag at ctt gag agt ttt cgc So92 Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg 475 Ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg ggt ctg Glu Ser Phe Arg 485 Ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg Cta tgt Si40 Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Cys 500 Ggc gcg gcg gta tta tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc Si88 Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg 505 Ccg ata Cac tat tct cag gat ggc atg atg aca gta gag tac tca cca gtc aca Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr 520 Gga aag cat ctt acg gat ggc atg aca gaa gaa tta tgc agg gct Si84 Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala	tctaaatac	ca ttcaaatatg	tatccgctca	tgagacaata	accctgataa atgcttcaa	t 4895
Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr 440 Ctg gtg aaa gta aaa gat gat gat Glu Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly 470 tac atc gaa ctg gat ctc aac agc ggt al Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg 485 Ccc gaa gaa cgt ttt cca atg ast gat ggt asg act ttt asc gat ggt asg agt ttt cgc Glu Ser Phe Arg 485 Ccc gaa gaa cgt ttt cca atg asg act ttt Leu Cys 500 Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys 500 Ggc gcg gta tta tcc cgt att gac gcc ggg caa gag caa ctc ggt asg agg caa ctc ggt asg agg caa ctc ggt asg agg caa ctc ggt all leu Ser Arg Ile Asp Ala Gly Gln Glu Glu Leu Gly Arg 515 Cgc ata cac tat tct cag aat gac ttg gtt gag tac tca cca gtc aca acc ggt asg aga aag cat ctc acc ggt asg aga aag cat ctc acc ggt asg aag aag aag aag aag aag aag aag aag	aatattgaa		Met Ser Ile	e Gln His Ph	ne Arg Val Ala Leu Il	
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Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg 485 ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt Si40 Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys 500 ggc gcg gta tta tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc Si88 Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg 505 cgc ata cac tat tct cag aat gac ttg gtt gag tac tca cca gtc aca Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr 520 ggaa aag cat ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala	Leu Val L	Lys Val Lys As	sp Ala Glu A	sp Gln Leu	Gly Ala Arg Val Gly	5044
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Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg 505 510 515 cgc ata cac tat tct cag aat gac ttg gtt gag tac tca cca gtc aca Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr 520 525 530 gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala	ccc gaa g Pro Glu G	Glu Arg Phe Pr	o Met Met S	er Thr Phe	Lys Val Leu Leu Cys	5140
Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr 520 525 530 gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct 5284 Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala	Gly Ala V	/al Leu Ser Ar	g Ile Asp A	cc ggg caa la Gly Gln	Glu Gln Leu Gly Arg	5188
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42

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His Ala Pro Arg Lys Lys Leu Phe Leu Ser Cys Ala Cys Leu Gly Leu 20 25 30

Ser Leu Ala Cys Leu Ser Ser Asn Ala Trp Ala Ser Val Glu Pro Leu 35 40 45

Ser Val Ser Gly Asn Lys Ile Tyr Ala Gly Glu Lys Ala Lys Ser Phe 50 55 60

Ala Gly Asn Ser Leu Phe Trp Ser Asn Asn Gly Trp Gly Glu Lys
70 75 80

Phe Tyr Thr Ala Asp Thr Val Ala Ser Leu Lys Lys Asp Trp Lys Ser 90 95

Ser Ile Val Arg Ala Ala Met Gly Val Gln Glu Ser Gly Gly Tyr Leu 100 105 110

Gln Asp Pro Ala Gly Asn Lys Ala Lys Val Glu Arg Val Val Asp Ala 115 120 125

Ala Ile Ala Asn Asp Met Tyr Val Ile Ile Asp Trp His Ser His Ser 130 135 140

Ala Glu Asn Asn Arg Ser Glu Ala Ile Arg Phe Phe Gln Glu Met Ala 145 150 155 160

- Arg Lys Tyr Gly Asn Lys Pro Asn Val Ile Tyr Glu Ile Tyr Asn Glu 165 170 175
- Pro Leu Gln Val Ser Trp Ser Asn Thr Ile Lys Pro Tyr Ala Glu Ala 180 185 190
- Val Ile Ser Ala Ile Arg Ala Ile Asp Pro Asp Asn Leu Ile Ile Val 195 200 205
- Gly Thr Pro Ser Trp Ser Gln Asn Val Asp Glu Ala Ser Arg Asp Pro 210 215 220
- Ile Asn Ala Lys Asn Ile Ala Tyr Thr Leu His Phe Tyr Ala Gly Thr 225 230 235 240
- His Gly Glu Ser Leu Arg Thr Lys Ala Arg Gln Ala Leu Asn Asn Gly 245 250 255
- Ile Ala Leu Phe Val Thr Glu Trp Gly Ala Val Asn Ala Asp Gly Asn 260 265 270
- Gly Gly Val Asn Gln Thr Asp Thr Asp Ala Trp Val Thr Phe Met Arg 275 280 285
- Asp Asn Asn Ile Ser Asn Ala Asn Trp Ala Leu Asn Asp Lys Ser Glu 290 295 300
- Gly Ala Ser Thr Tyr Tyr Pro Asp Ser Lys Asn Leu Thr Glu Ser Gly 305 310 315 320
- Lys Ile Val Lys Ser Ile Ile Gln Ser Trp Pro Tyr Lys Ala Gly Ser 325 330 335
- Ala Ala Ser Thr Thr Thr Asp Gln Ser Thr Asp Thr Thr Met Ala Pro 340 345 350
- Pro Leu Thr Asn Arg Pro Gln Pro Thr His Arg Gln Thr Ala Asp Cys 355 360 365
- Cys Asn Ala Asn Val Tyr Pro Asn Trp Val Ser Lys Asp Trp Ala Gly 370 375 380

Arg Gln Arg Leu Ile Thr Lys Gln Ala Asn Arg Ser Ser Thr Lys Gly 385 390 395 400

Thr Cys Ile Pro Gln Thr Gly Thr Leu His Pro Phe Arg Ala Ala Ile 405 410 415

Pro Pro Gly His Arg Leu Val Ala Val Thr Asn 420 425

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<211> 286

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Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser 85 90 95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
100 105 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu 145 150 155 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg 165 170 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp 195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp 275 280 285

<210> 24

<211> 396

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic amino acid sequence

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Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu 1 5 10 15

Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly Leu Leu 20 25 30

Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly Val Leu 35 40 45

Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val Leu Gly 50 55 60

Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu 65 70 75 80

Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro Val Leu 85 90 95

Trp Ile Leu Tyr Ala Gly Arg Ile Val Ala Gly Ile Thr Gly Ala Thr 100 105 110

Gly Ala Val Ala Gly Ala Tyr Ile Ala Asp Ile Thr Asp Gly Glu Asp 115 120 125

Arg Ala Arg His Phe Gly Leu Met Ser Ala Cys Phe Gly Val Gly Met 130 135 140

Val Ala Gly Pro Val Ala Gly Gly Leu Leu Gly Ala Ile Ser Leu His 145 150 150 160

Ala Pro Phe Leu Ala Ala Ala Val Leu Asn Gly Leu Asn Leu Leu 175

Gly Cys Phe Leu Met Gln Glu Ser His Lys Gly Glu Arg Arg Pro Met 180 185 190

Pro Leu Arg Ala Phe Asn Pro Val Ser Ser Phe Arg Trp Ala Arg Gly 195 200 205

Met Thr Ile Val Ala Ala Leu Met Thr Val Phe Phe Ile Met Gln Leu 210 220

Val Gly Gln Val Pro Ala Ala Leu Trp Val Ile Phe Gly Glu Asp Arg 225 230 235 240

Phe Arg Trp Ser Ala Thr Met Ile Gly Leu Ser Leu Ala Val Phe Gly 245 250 255

Ile Leu His Ala Leu Ala Gln Ala Phe Val Thr Gly Pro Ala Thr Lys 260 265 270 Arg Phe Gly Glu Lys Gln Ala Ile Ile Ala Gly Met Ala Ala Asp Ala 275 280 285

Leu Gly Tyr Val Leu Leu Ala Phe Ala Thr Arg Gly Trp Met Ala Phe 290 295 300

Pro Ile Met Ile Leu Leu Ala Ser Gly Gly Ile Gly Met Pro Ala Leu 305 310 315 320

Gln Ala Met Leu Ser Arg Gln Val Asp Asp Asp His Gln Gly Gln Leu 325 330 335

Gln Gly Ser Leu Ala Ala Leu Thr Ser Leu Thr Ser Ile Thr Gly Pro 340 345 350

Leu Ile Val Thr Ala Ile Tyr Ala Ala Ser Ala Ser Thr Trp Asn Gly 355 360 365

Leu Ala Trp Ile Val Gly Ala Ala Leu Tyr Leu Val Cys Leu Pro Ala 370 375 380

Leu Arg Arg Gly Ala Trp Ser Arg Ala Thr Ser Thr 385 390 395